

In the Claims

The listing of claims will replace all prior versions and listing, of claims in the application:

Listing of Claims:

1. (Original) A method of selecting a plant having enhanced transpiration efficiency, comprising detecting a genetic marker for transpiration efficiency which marker comprises a nucleotide sequence linked genetically to an ERECTA locus in the genome of the plant and selecting a plant that comprises or expresses the genetic marker.
2. (Original) The method according to claim 1 wherein the genetic marker comprises an ERECTA allele or erecta allele, or a protein-encoding portion thereof.
3. (Original) The method according to claim 2 wherein the genetic marker comprises a nucleotide sequence having at least about 55% overall sequence identity to at least about 20 nucleotides in length of any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11 to 19 or 21 to 44 or a complementary sequence thereto.
4. (Currently Amended) The method according to claim 2 ~~or 3~~ wherein the genetic marker comprises a nucleotide sequence selected from the group consisting of:
 - (a) a sequence having at least about 55% identity to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32 SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID

NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38;
SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID
NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44;

- (b) a sequence encoding an amino acid sequence having at least about 55% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 20 and SEQ ID NO: 45; and
 - (c) a sequence complementary to (a) or (b).
5. (Currently Amended) The method according to ~~any one of claims 1 to 4~~ claim 1 wherein the plant is selected from the group consisting of Arabidopsis thaliana, rice, sorghum, wheat and maize.
6. (Currently Amended) The method according to ~~any one of claims 1 to 5~~ claim 1 comprising linking the transpiration efficiency phenotype of the plant to the expression of the marker in the plant.
7. (Currently Amended) The method according to ~~any one of claims 1 to 5~~ claim 1 comprising linking a structural polymorphism in DNA to a transpiration efficiency phenotype in the plant.
8. (Original) The method according to claim 7 wherein the polymorphism is determined by a process comprising detecting a restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), single strand chain polymorphism (SSCP) or microsatellite analysis.
9. (Currently Amended) The method according to ~~any one of claims 1 to 8~~ claim 1 comprising hybridizing a probe or primer of at least about 20 nucleotides in length from any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11 to 19 or 21 to 44 or a complementary sequence thereto to genomic DNA

from the plant, and detecting the hybridization using a detection means.

10. (Currently Amended) The method according to ~~any one of claims 1 to 9~~ claim 1 wherein the selected plant has enhanced transpiration efficiency compared to a near-isogenic plant that does not comprise or express the genetic marker.
11. (Original) A method of selecting a plant having enhanced transpiration efficiency, comprising:
 - (a) screening mutant or near-isogenic or recombinant inbred lines of plants to segregate alleles at an ERECTA locus;
 - (b) identifying a polymorphic marker linked to said ERECTA locus; and
 - (c) selecting a plant that comprises or expresses the marker.
12. (Original) A method of modulating the transpiration efficiency of a plant comprising introducing an isolated ERECTA gene or an allelic variant thereof or the protein-encoding region thereof to a plant and selecting a plant having a different transpiration efficiency compared to a near-isogenic plant that does not comprise the introduced ERECTA gene or allelic variant or protein-encoding region.
13. (Original) The method according to claim 12 wherein the ERECTA gene or allelic variant or protein-encoding region comprises a nucleotide sequence selected from the group consisting of:
 - (a) a sequence having at least about 55% identity to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19; SEQ ID

NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24,
SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID
NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31,
SEQ ID NO: 32 SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID
NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38;
SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID
NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44; and

- (b) a sequence encoding an amino acid sequence having at least about 55% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 20 and SEQ ID NO: 45.

14. (Currently Amended) The method according to claim 12 ~~or 13~~ wherein the plant is selected from the group consisting of Arabidopsis thaliana, rice, sorghum, wheat and maize.
15. (Currently Amended) The method according to ~~any one of claims 12 to 14~~ claim 12 wherein the ERECTA gene or allelic variant or protein-encoding region is introduced to the plant by a process comprising introgression.
16. (Currently Amended) The method according to ~~any one of claims 12 to 14~~ claim 12 wherein the ERECTA gene or allelic variant or protein-encoding region is introduced to the plant by a process comprising transforming plant material with a gene construct comprising the gene or allelic variant or protein-encoding region thereof.
17. (Currently Amended) The method according to ~~any one of claims 12 to 16~~ claim 12 further comprising expressing the introduced gene or allelic variant or protein encoding region in the plant.
18. (Currently Amended) The method according to ~~any one of claims 12 to 17~~ claim 12 wherein transpiration efficiency is enhanced in the plant.

19. (Original) The method of claim 18 wherein the transpiration efficiency is enhanced as a consequence of the ectopic expression of an *ERECTA* allele or the protein-encoding region thereof in the plant.
20. (Currently Amended) The method according to ~~any one of claims 12 to 17~~ claim 12 wherein transpiration efficiency is reduced in the plant.
21. (Original) The method of claim 20 wherein the transpiration efficiency is reduced as a consequence of reduced expression of an *ERECTA* allele in the plant.
22. (Currently Amended) A plant having modified transpiration efficiency compared to a near-isogenic plant wherein said plant is produced by a process comprising performing the method according to ~~any one of claims 12 to 21~~ claim 12.
23. (Original) The plant of claim 22 selected from the group consisting of a rice plant, a wheat plant and a maize plant.
24. (Currently Amended) An isolated *ERECTA* gene from wheat capable of determining or modulating the transpiration efficiency of a plant wherein said isolated *ERECTA* gene comprises ~~comprising~~ a nucleotide sequence selected from the group consisting of:
 - (i) a sequence selected from the group consisting of: SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19;
 - (ii) a sequence encoding the amino acid sequence set forth in SEQ ID NO: 20; and
 - (iii) a sequence that is complementary to (i) or (ii).

25. (Currently Amended) An isolated *ERECTA* gene from maize capable of determining or modulating the transpiration efficiency of a plant wherein said isolated *ERECTA* gene comprises ~~comprising~~ a nucleotide sequence selected from the group consisting of:

- (i) a sequence selected from the group consisting of: SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38; SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43 and SEQ ID NO: 44;
- (ii) a sequence encoding the amino acid sequence set forth in SEQ ID NO: 45; and
- (iii) a sequence that is complementary to (i) or (ii).

26-36. (Canceled)